

FIG. 2A

FIG. 2A

1 gcgagcgag cggagcctgg agagaaggcg ctgggctgag agggcgaggg ggcgcgaggg cagggggcaa cggaccccg
81
ccgcacccc atg gcg ccc gtc gcc gtc tgg gcc gcg ctg ggc gtc gga ctg gag ctc tgg gct gcg
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
147 -22
gcg cac gcc ttg ccc gcc cag gtg gca ttt aca ccc tac gcc ccg gag ccc ggg agc aca tgc cgg
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
213 -1 +1
ctc aga gaa tac tat gac cag aca gct cag atg tgc agc aaa tgc tgc ccg gcc caa cat gca
Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala
279
aaa gtc ttc tgt acc aag acc tgc gac acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag
Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
345
ctc tgg aac tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct gac cag gtg gaa act
Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr
411
caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc agc ccc ggc tgg tac tgc gcg ctg agc
Gln Ala Cys Thr Arg Glu Gln Asn Arg ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
477
aag cag gag ggg tgc cgg ctg tgc ggc cgg ctg cgc aag tgc cgc ccg gcc ttc ggc gtg gcc aga
Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg
543
cca gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc cgg ggg acg ttc ttc aac acg act
Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr
609
tca tcc acg gat att tgc agg ccc cac cag atc tgt aac gtg gtc gcc atc ccc ggg aat gca agc
Ser Ser Thr Asp Ile Cys Arg Pro His Gln ile Cys Asn Val Val Ala ile Pro Gly Asn Ala Ser
675
atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta cac tta ccc
Met Asp Ala Val Cys Thr Ser Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro
741
186

TBPII

TRANSMEMBRANE

DOMAIN

FIG. 2C

1545 cctgggtcctt ccaggccccc accactagga ctctgaggct ctttctgagg caagttcctc tagtgccctc cacagccgca
gcctccctct gacctgcagg ccaagagcag aggcagcgag ttggggaaaag cctctgctgc catgggtgtgt ccctctcgga
aggctggctg ggcatggacg ttccggggcat gctgggggcaa gtccctgact ctctgtgacc tgccccgccc agctgcacct
gccagcctgg ctctctggagc ccttgggttt ttgtttgtt ttgtttgtt tctccccctg ggctctgccc
agctctggct tccagaaaac ccagcatcc ttttctgcag aggggctttc tggagaggag ggatgctgcc tgagtcaccc
atgaagacag gacagtgtt ctgcctgagg cagagactgc gggatggtec tggggctctg tgtagggagg aggtggcagc
cctgtaggga acggggtcct tcaagttagc tcaggaggct tggaaagcat cacctcaggc caggtgcagt ggctcacgcc
tatgatccca gcactttggg aggtgaggc ggttggatca cctgagggtta ggagttcgag accagcctgg ccaacatggt
aaaaccccat ctctactaaa aatacagaaa ttagccgggc3683
acctcaggc caggtgcagt ggctcacgcc
2075

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

FIG. 3

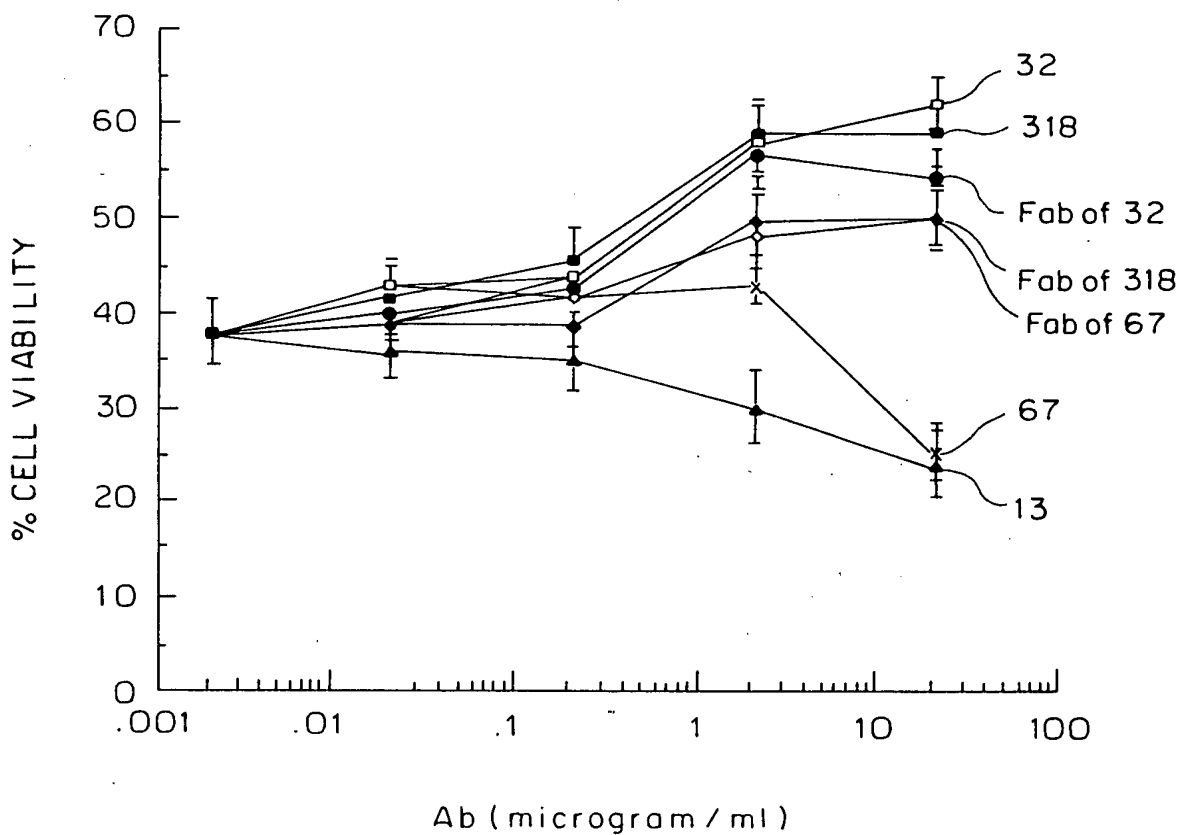


FIG. 4

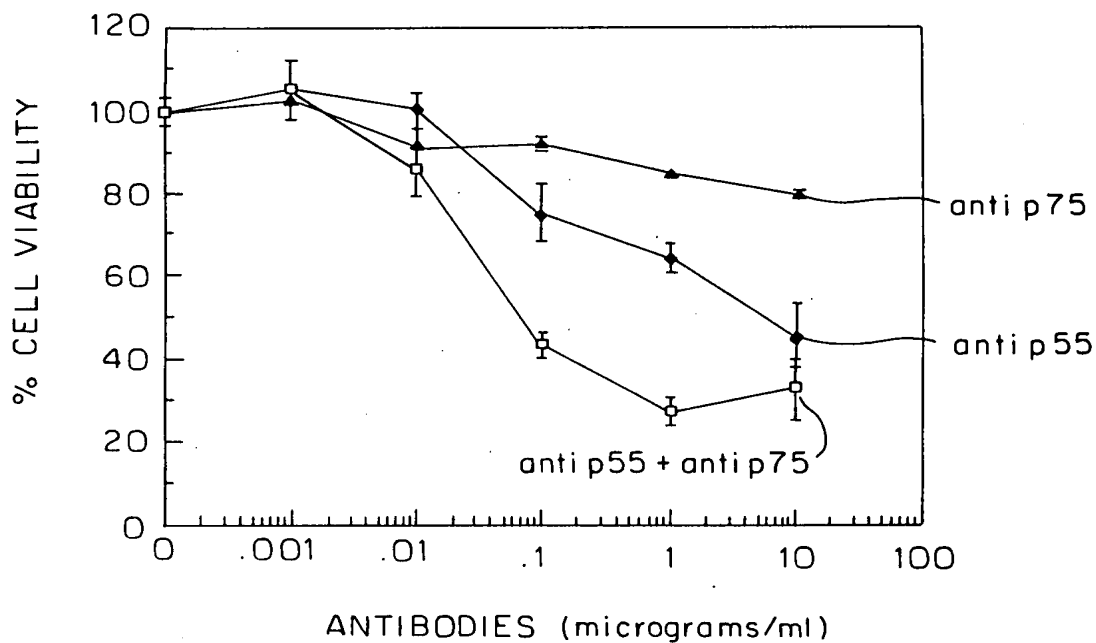


FIG. 5

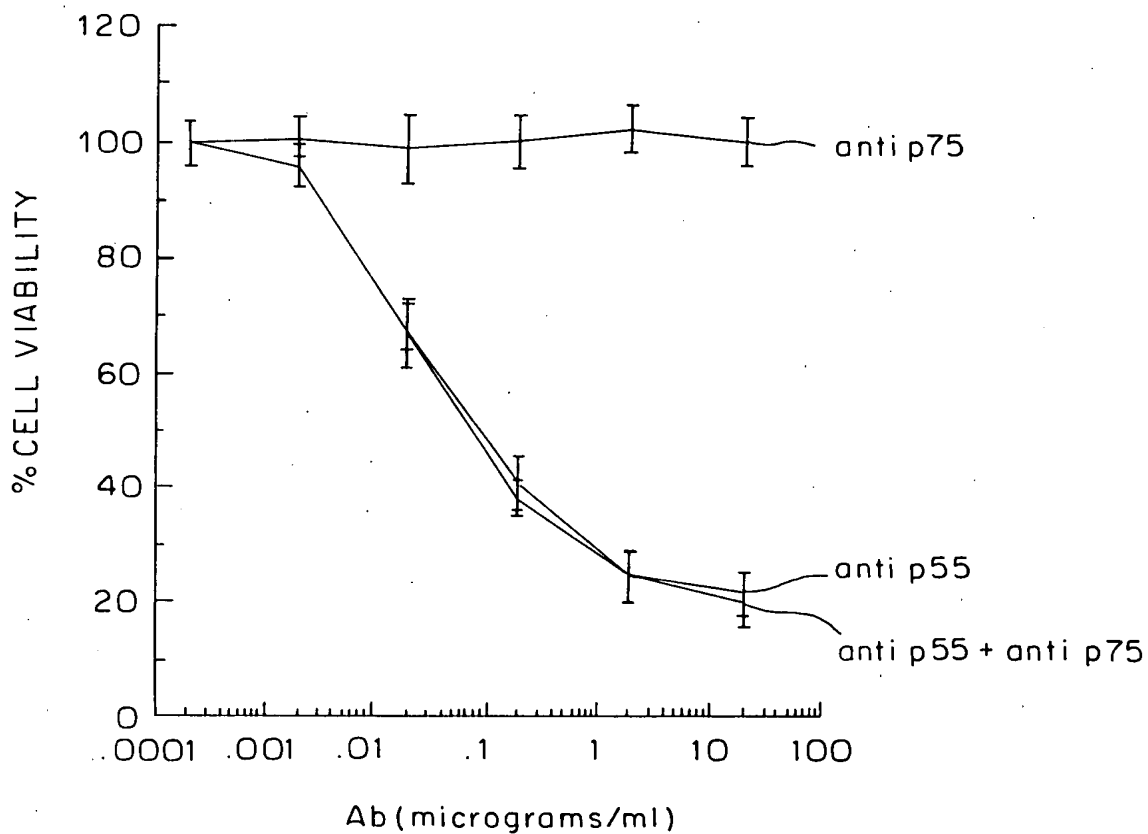


FIG. 6

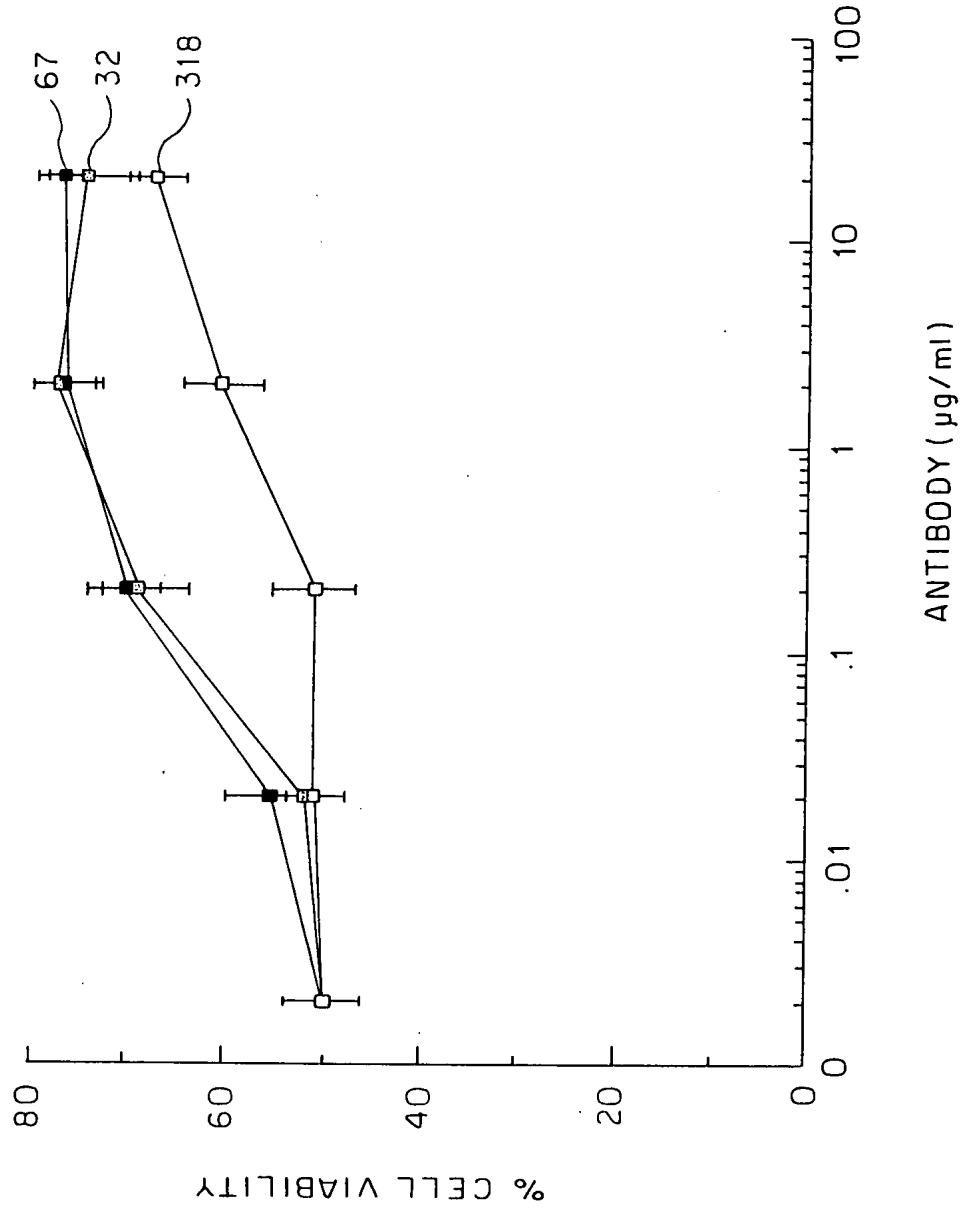


FIG. 7

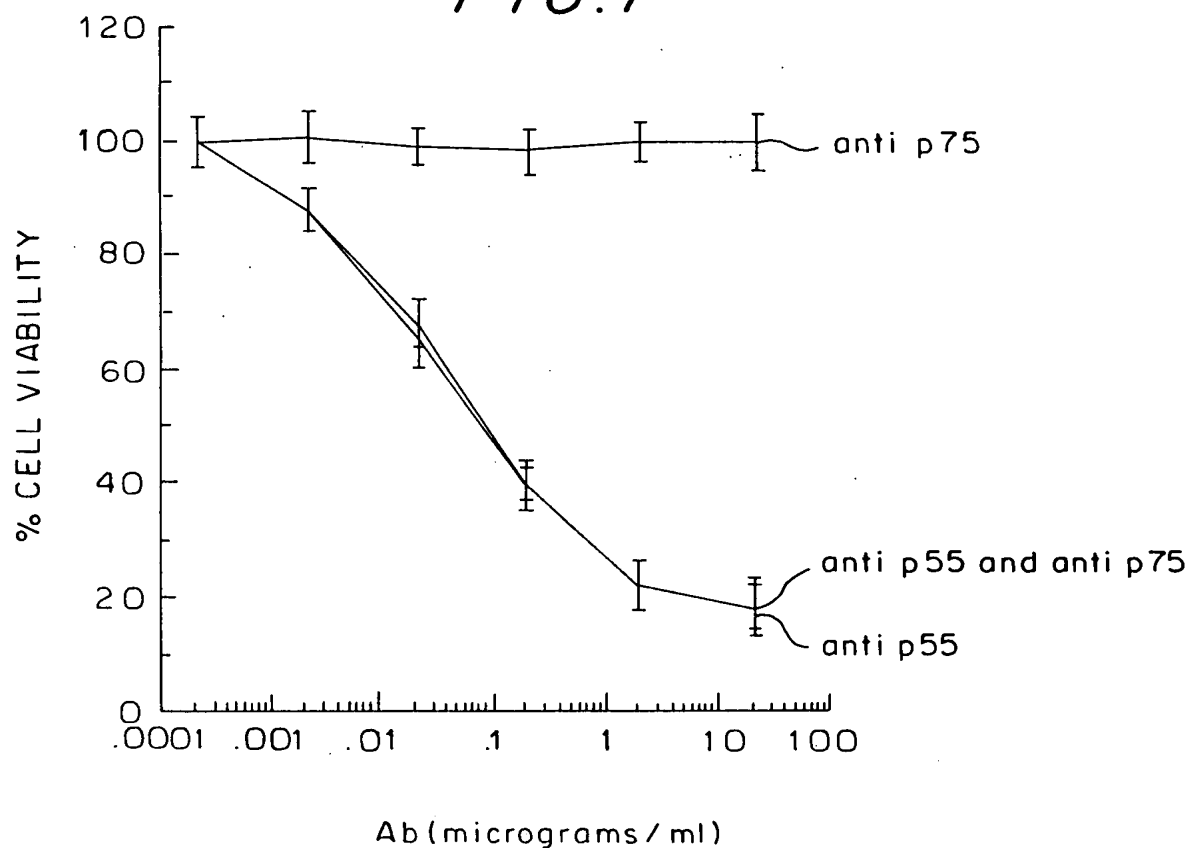


FIG. 8

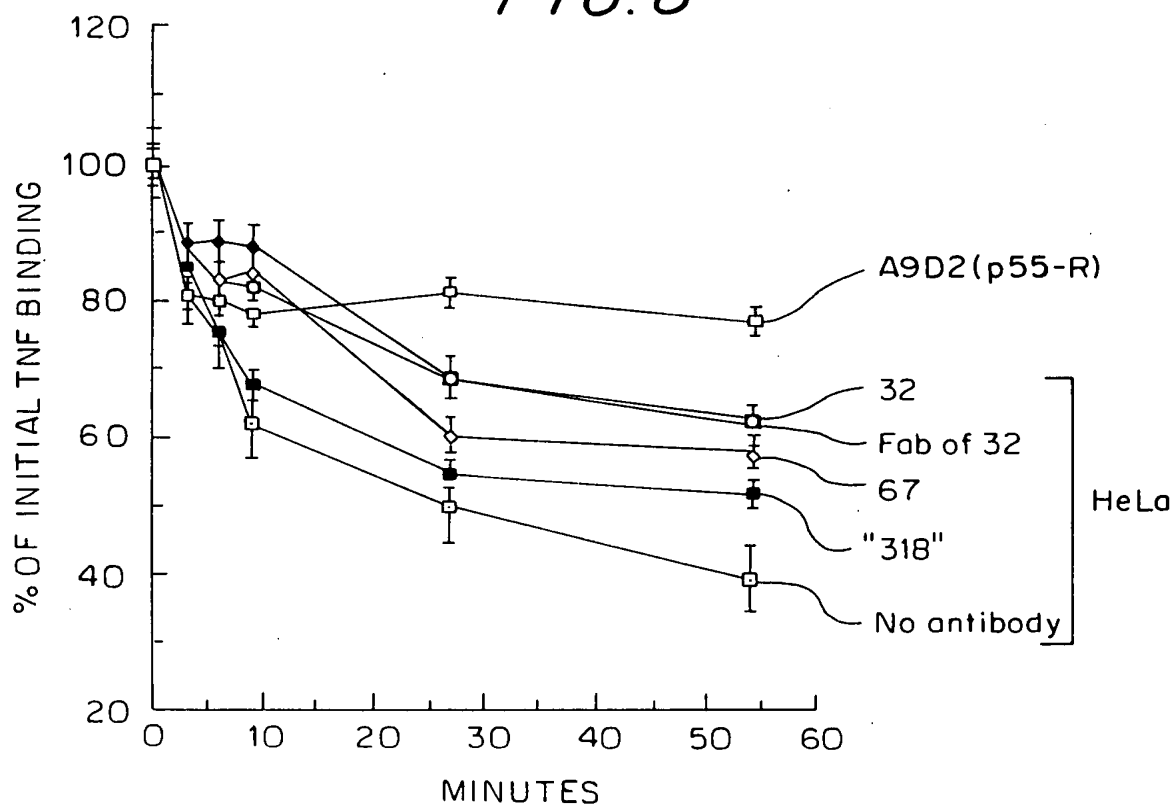


FIG. 9

FIG. 9

hu p55	TNF-R (3-42)	VCPQGGKYYIHQPQNN-----SICC-TKCHKGTYLYND--CPGPGQDTTDCR
hu p75	TNF-R (39-76)	TCRLREYD-QTA-----QMCC-SKCSFGQHAKVF--CTKTS-DTVCDC
hu FAS	(31-67)	QNLGLH-HDGF-----CH-KPCPPGERKARD--CTVNGDEPDCV
hu NGF-R	(3-37)	ACPTGLYTHSGE-----CC-KACNLGEGVAQP--CGA-NQTVCE
hu CDw40	(25-60)	ACREKQYLINSQ-----CC-SLCPGQKLVSD--CTEF-TETECCL
rat Ox40	(25-60)	NCVKDTYPSGHK-----CC-RECPGHHGMVSR--CDHT-RDTVCH
hu p55	TNF-R (43-86)	ECESGSEFTASEHHL-RHCLSLSC-SKCRKENQVEISSCTVD-RDTVCG
hu p75	TNF-R (77-119)	SCEDSTYTQLWNWV-PECLSCGSRCSDD--QVETQACTRE-QNRICT
hu FAS	(68-112)	PCQEGKEYTDKAHFSSKRRRC-RLCDEGHGLEVEINCTRT-QNTKCR
hu NGF-R	(38-80)	PCLDSTVSSDVVSATEPCPC-TECVGLQSHSAP--CVEA-DDAVCR
hu CDw40	(61-104)	PCGSEFLDTHRETN-CHQH-KYCDPNLGLRVQKGTSE-TDTICT
rat Ox40	(61-104)	PC-EPGEYNEAVNY-DTCKQC-TQCNHRSGSELKQNTPT-EDTVCQ
hu p55	TNF-R (87-126)	-CRKNQYRHYWSENLFQCFNC--SLCLHGT-VHLSQCEK-QNTVC-
hu p75	TNF-R (120-162)	-CRPGWYCA--LSKQEGCRLCAPIRKCRPGFGVAPGTET-SDVVCK
hu FAS	(113-149)	-CKPNFFCN--STVCEHCDPC--TKCEHGI-IKE-CTLT-SNTKC-
hu NGF-R	(81-119)	-CAYGYQD--ETTGRCEAC--RVCEAGSGLVFSQDK-QNTVCE
hu CDw40	(105-144)	-CEEGWHC-----TSEACESVLHRSQSPGFGVKQIATGV-SDTICE
rat Ox40	(105-123)	-CREGTQP-----RQDS-----SHKLGV-----CV
hu p55	TNF-R (127-155)	THAGFFLR--ENE---CVSC-SNCKKSL-----ECTK-----LC-
hu p75	TNF-R (163-201)	PCAPGTFSTTSST-DICRPH-QICN-----VVA--IPGNASMDAVCT
hu NGF-R	(120-161)	ECPDGTSDEAHV-DPCLPC-TVCEATERQLR--ECTRW-ADAECE
hu CDw40	(145-186)	PCPVGFFSNVSSAF-EKCHP--TSCETKDLVVQ--QAGTNKTDVTCG
rat Ox40	(124-164)	PCPPGHFSPGSHQ---ACKPW-TNCTLSGKQIR--HPASNSLDTVCE